

Fig. 1

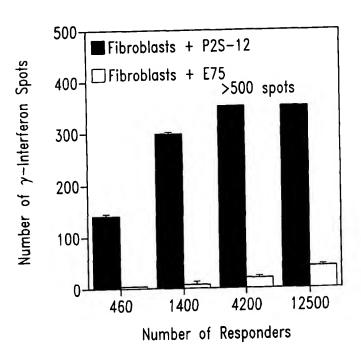


Fig. 2A

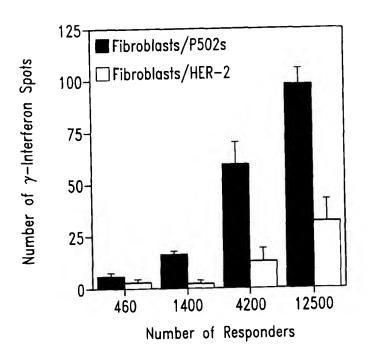
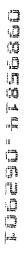
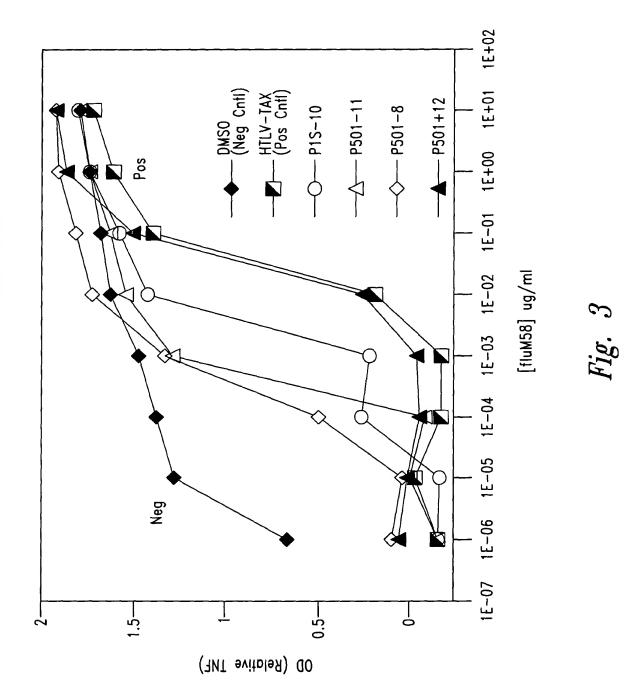


Fig. 2B





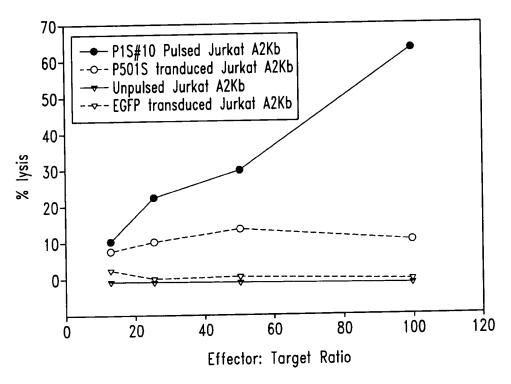


Fig. 4

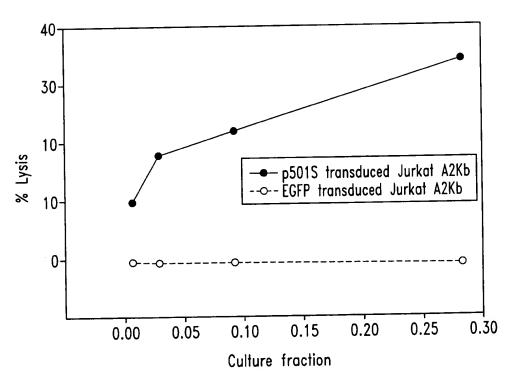
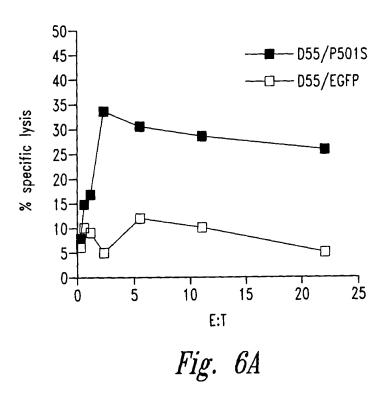
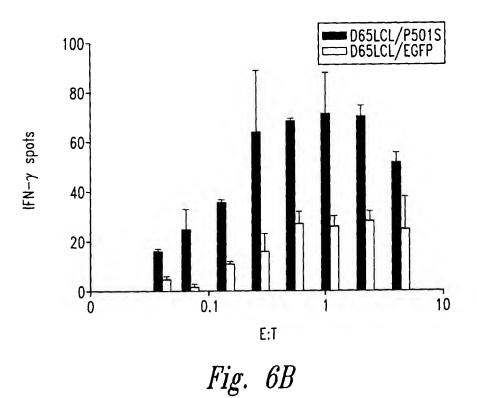
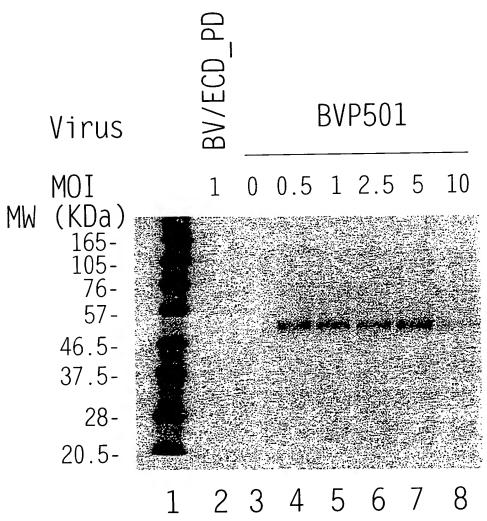


Fig. 5





## Expression of P501S by the Baculovirus Expression System



0.6 million high 5 cells in 6-well plate were infected with an unrelated control virus BV/ECD\_PD (lane2), without virus (lane3), or with recombinant baculovirus for P501 at different MOIs (lane 4-8). Cell lysates were run on SDS-PAGE under the reducing conditions and analyzed by Western blot with a monoclonal antibody against P501S (P501S-10E3-G4D3). Lane 1 is the biotinylated protein molecular weight marker (BioLabs).

1250 527 All other peptides /TAYMVSAA FIGURE 8. Mapping of the epitope recognized by 10E3-G4-D3 500 7 ng 10E3 250 0.5 2.5. 1.5 39APFPNGHVGAGGSGLLPPPA459 .a.o 097 525 553 343 P501S fragment used for immunization: Transmembrane domain P501S sequence Full-length P501S:

## Schematic of P501S with predicted transmembrane, cytoplasmic, and extracellular regions

MVQRLWVSRLLRHRK AQLLLVNLLTFGLEVCLAAGIT YVPPLLLEVGVEEKFM TMVLGIGPVLGLVCYPLLGSAS

DHWRGRYGRRP FIWALSLGILLSLFLIPRAGWL AGLLCPDPRPLE LALLILGVGLLDFCGQVCFTPL

EALLSDLFRDPDHCRQ AYSVYAFMISLGGCLGYLLPAI DWDTSALAPYLGTQEE

CLFGLLTLIFLTCVAATLLV AEEAALGPTEPAEGLSAPSLSPHCCPCRARLAFRNLGALLPRL

HQLCCRMPRTLRR LFVAELCSWMALMTFTLFYTDF VGEGLYQGVPRAEPGTEARRHYDEGVR

MGSLGLFLQCAISLVFSLVM DRLVQRFGTRAVYLAS VAAFPVAAGATCLSHSVAVVTA SAA

LTGFTFSALQILPYTLASLY HREKQVFLPKYRGDTGGASSEDSLMTSFLPGPKPGAPFPNGHVGAGGSGL

LPPPPALCGASACDVSVRVVVGEPTEARVVPGRG ICLDLAILDSAFLLSQVAPSLF MGSIVQLSQS

VTAYMVSAAGLGLVAIYFAT QVVFDKSDLAKYSA

<u>Underlined sequence</u>: Predicted transmembrane domain; **Bold sequence**: Predicted extracellular domain; *Italic sequence*: Predicted intracellular domain. Sequence in bold/underlined: used generate polyclonal rabbit serum

Localization of domains predicted using HMMTOP (G.E. Tusnady an I. Simon (1998) Principles Governing Amino Acid Composition of Integral Membrane Proteins: Applications to topology Prediction.J.Mol Biol. 283, 489-506.

Genomic Map of (5) Corixa Candidate Genes

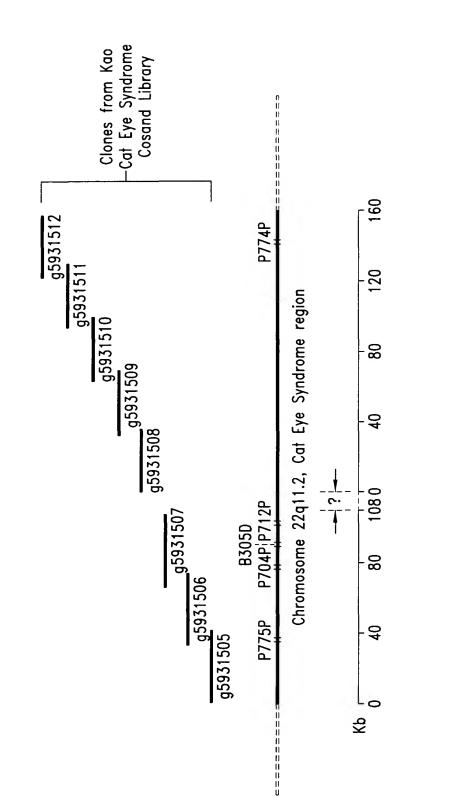


Fig. 10

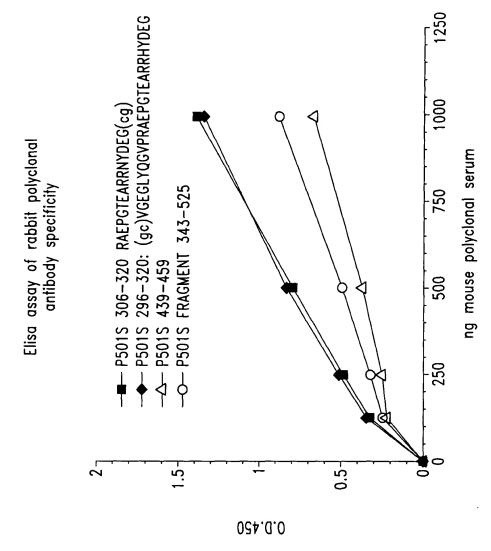


Fig. 11